

OIIPE

RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/870,122

TIME: 10:25:07

Input Set : A:\PCT-US99-28826 Sequence listing.txt

Output Set: N:\CRF3\11212001\I870122.raw

ENTERED

4 <110> APPLICANT: Regents of the University of Minnesota et al.
6 <120> TITLE OF INVENTION: Streptococcal C5a peptidase vaccine
8 <130> FILE REFERENCE: 600.450W01
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/870,122
C--> 10 <141> CURRENT FILING DATE: 2001-05-30
10 <150> PRIOR APPLICATION NUMBER: US 09/206,898
11 <151> PRIOR FILING DATE: 1998-12-07
13 <150> PRIOR APPLICATION NUMBER: US 08/589,756
14 <151> PRIOR FILING DATE: 1996-01-22
16 <160> NUMBER OF SEQ ID NOS: 23
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1164
22 <212> TYPE: PRT
23 <213> ORGANISM: Streptococcus pyogenes
25 <400> SEQUENCE: 1
26 Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
27 1 5 10 15
28 Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
29 20 25 30
30 Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Ala Val Glu Thr Pro
31 35 40 45
32 Gln Pro Thr Thr Val Ser Glu Val Pro Ser Ser Lys Glu Thr Lys
33 50 55 60
34 Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Val Ala Asp Asp Ala
35 65 70 75 80
36 Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Pro Asp Thr Ser Ala
37 85 90 95
38 Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
39 100 105 110
40 Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
41 115 120 125
42 Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
43 130 135 140
44 Lys Ala Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
45 145 150 155 160
46 Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
47 165 170 175
48 Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
49 180 185 190
50 His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
51 195 200 205
52 Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
53 210 215 220
54 Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
55 225 230 235 240
56 Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val

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57          245          250          255
58   Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
59          260          265          270
60   Asp Glu Thr Lys Lys Pro Phe Val Tyr Ala Lys Ser Lys Gly Val Arg
61          275          280          285
62   Ile Val Thr Thr Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
63          290          295          300
64   Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
65          305          310          315          320
66   Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Asn Gln
67          325          330          335
68   Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu
69          340          345          350
70   Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
71          355          360          365
72   Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val
73          370          375          380
74   Lys Gly Lys Ile Ala Leu Ile Glu Arg Ser Asp Ile Asp Phe Thr Asp
75          385          390          395          400
76   Lys Ile Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
77          405          410          415
78   Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
79          420          425          430
80   Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
81          435          440          445
82   Asn Ser Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
83          450          455          460
84   Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
85          465          470          475          480
86   Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
87          485          490          495
88   Leu Ser Ser Ala Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
89          500          505          510
90   Met Ser Ala Pro Leu Val Ala Val Ile Met Gly Leu Leu Gln Lys Gln
91          515          520          525
92   Tyr Glu Thr Gln Tyr Pro Asp Met Thr Gln Ser Glu Arg Leu Asp Leu
93          530          535          540
94   Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
95          545          550          555          560
96   Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
97          565          570          575
98   Ala Lys Lys Ala Ser Glu Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
99          580          585          590
100  Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
101          595          600          605
102  Thr Val Thr Val His Asn Lys Ser Asp Lys Pro His Glu Leu Tyr Tyr
103          610          615          620
104  Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
105          625          630          635          640

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```

106  Ala Pro Lys Ala Leu Ile Glu Thr Ser Trp Gln Lys Ile Thr Ile Pro
107                645                650                655
108  Ala Asn Ser Ser Lys Gln Val Thr Ile Pro Ile Asp Ile Ser Gln Phe
109                660                665                670
110  Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
111                675                680                685
112  Phe Val Arg Ile Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile
113                690                695                700
114  Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
115                705                710                715                720
116  Lys Pro Leu Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Glu
117                725                730                735
118  Ile Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
119                740                745                750
120  Ala Leu Lys Asn Asp Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
121                755                760                765
122  Thr Ile Ile Asn Val Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
123                770                775                780
124  Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
125                785                790                795                800
126  Gln Asp Asp Asp Arg His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
127                805                810                815
128  Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
129                820                825                830
130  Gln Phe His Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
131                835                840                845
132  Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
133                850                855                860
134  Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
135                865                870                875                880
136  Thr Arg Phe Glu Ile Ser Arg Trp Asp Gly Lys Asp Lys Asp Ala Lys
137                885                890                895
138  Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
139                900                905                910
140  Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
141                915                920                925
142  Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
143                930                935                940
144  Arg Arg Leu Thr Leu Ala Ser Lys Pro Gln Thr Ser Gln Pro Val Tyr
145                945                950                955                960
146  Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
147                965                970                975
148  Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
149                980                985                990
150  Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
151                995                1000                1005
152  Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
153                1010                1015                1020
154  Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser

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```

155      1025      1030      1035      1040
156  Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Gln Asp Gly
157      1045      1050      1055
158  Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Thr Lys Pro Gly Gln Asp
159      1060      1065      1070
160  Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Lys
161      1075      1080      1085
162  Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Pro
163      1090      1095      1100
164  Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys
165      1105      1110      1115      1120
166  Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr Asn
167      1125      1130      1135
168  Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Leu Gly Leu
169      1140      1145      1150
170  Val Ala His Ile Phe Lys Thr Lys Arg Thr Glu Asp
171      1155      1160
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 1167
175 <212> TYPE: PRT
176 <213> ORGANISM: Streptococcus pyogenes
178 <400> SEQUENCE: 2
179  Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
180    1          5          10          15
181  Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
182      20          25          30
183  Thr Val Thr Glu Asp Thr Pro Val Thr Glu Gln Ala Val Glu Thr Pro
184      35          40          45
185  Gln Pro Thr Ala Val Ser Glu Glu Val Pro Ser Ser Lys Glu Thr Lys
186      50          55          60
187  Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Ile Ala Asp Asp Ala
188      65          70          75          80
189  Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
190      85          90          95
191  Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
192      100         105         110
193  Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
194      115         120         125
195  Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
196      130         135         140
197  Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
198      145         150         155         160
199  Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
200      165         170         175
201  Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
202      180         185         190
203  His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
204      195         200         205
205  Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu

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206	210	215	220
207	Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg		
208	225	230	235
209	Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val		
210	245	250	255
211	Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro		
212	260	265	270
213	Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser		
214	275	280	285
215	Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg		
216	290	295	300
217	Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala		
218	305	310	315
219	Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln		
220	325	330	335
221	Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu		
222	340	345	350
223	Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp		
224	355	360	365
225	Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val		
226	370	375	380
227	Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp		
228	385	390	395
229	Lys Val Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr		
230	405	410	415
231	Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln		
232	420	425	430
233	Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp		
234	435	440	445
235	Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro		
236	450	455	460
237	Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr		
238	465	470	475
239	Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile		
240	485	490	495
241	Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser		
242	500	505	510
243	Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln		
244	515	520	525
245	Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu		
246	530	535	540
247	Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp		
248	545	550	555
249	Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp		
250	565	570	575
251	Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn		
252	580	585	590
253	Thr Ser Ser Lys Val His Leu Asn Val Ser Asp Lys Phe Glu Val		
254	595	600	605

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/870,122

DATE: 12/05/2001

TIME: 10:25:08

Input Set : A:\PCT-US99-28826 Sequence listing.txt.txt

Output Set: N:\CRF3\11212001\I870122.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date